

IN THE SPECIFICATION:

Kindly replace the paragraph beginning at Page 19, line 25 with the following paragraph:

Laminin $\alpha 4$ gene-specific polynucleotides, including laminin $\alpha 4$ -specific mRNA species, are determined by base sequence similarity or homology to known mammalian laminin $\alpha 4$ -specific nucleotide sequences. Base sequence homology is determined by conducting a base sequence similarity search of a genomics data base, such as the GenBank database of the National Center for Biotechnology Information (~~NCBI~~; ~~www.ncbi.nlm.nih.gov/BLAST/~~), using a computerized algorithm, such as PowerBLAST, QBLAST, PSI-BLAST, PHI-BLAST, gapped or ungapped BLAST, or the "Align" program through the Baylor College of Medicine server (~~www.hgsc.bcm.tmc.edu/seq_data~~). (E.g., Altschul, S.F., *et al.*, *Gapped BLAST and PSI-BLAST: a new generation of protein database search programs*, Nucleic Acids Res. 25(17):3389-402 [1997]; Zhang, J., & Madden, T.L., *PowerBLAST: a new network BLAST application for interactive or automated sequence analysis and annotation*, Genome Res. 7(6):649-56 [1997]; Madden, T.L., *et al.*, *Applications of network BLAST server*, Methods Enzymol. 266:131-41 [1996]; Altschul, S.F., *et al.*, *Basic local alignment search tool*, J. Mol. Biol. 215(3):403-10 [1990]). Preferably, a laminin $\alpha 4$ -specific polynucleotide sequence, including an mRNA sequence, is at least 5 to 30 contiguous nucleotides long, more preferably at least 6 to 15 contiguous nucleotides long, and most preferably at least 7 to 10 contiguous nucleotides long. Preferably, the laminin $\alpha 4$ -specific mRNA is at least about 45 contiguous nucleotides long. A laminin $\alpha 4$ -specific mRNA can be, but is not necessarily, an mRNA species containing a nucleotide sequence that encodes a functional laminin $\alpha 4$ subunit or a fragment thereof. Also included among laminin $\alpha 4$ -specific mRNAs are splice variants.